

09/596,746.

PATENT APPLICATION
Attorney's Docket No.: 2631.1002-001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Raymond J. Dattwyler, Gerald Seinost, Daniel Dykhuizen, Benjamin J. Luft,
Maria J.C. Gomes-Solecki

C 8 C
EME

Issued: June 13, 2006

Patent No.: 7,060,281 B1

Title: GROUPS OF BORRELIA BURGDORFERI AND BORRELIA AFZELII
THAT CAUSE LYME DISEASE IN HUMANS

CERTIFICATE OF MAILING OR TRANSMISSION

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Katie Norris

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REQUEST FOR CERTIFICATE OF CORRECTION

Office of Publications
Certificate of Corrections Branch
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

Pursuant to 35 U.S.C. § 254, we hereby request a Certificate of Correction be issued for the above-referenced U.S. Letters Patent for the following reasons:

SEQ ID NOS. 53-86 were not included in the issued patent, even though they were properly entered in a Substitute Sequence Listing filed on September 22, 2005. Certain of the claims recite SEQ ID NOS that are not in the published patent, which will be confusing for the public.

Certificate
JUN 28 2007
of Correction

Since the errors were made by the U.S. Patent and Trademark Office and not by Patentees or Patentee's Attorney/Agent, it is understood that there are no additional fees for the requested Certificate of Correction. A Certificate of Correction is enclosed herewith.

Respectfully submitted,

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Elizabeth W. Mata
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Telephone: (978) 341-0036
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Dated: June 22, 2001

UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 7,060,281 B1

DATED : June 13, 2006

INVENTOR(S) : Raymond J. Dattwyler, Gerald Steinost, Daniel
Dykhuizen, Benjamin J. Luft, Maria J.C. Gomes-Solecki

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

At Column 45, Insert SEQ ID NOS. 53-86 after SEQ ID NO: 52

<210> 53

<211> 1137

<212> DNA

<213> ospC Chimera

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<222> (1)...(1137)

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No. of add'l copies
@ 50¢ per page



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Pro
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7,060,281 B1

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Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
145 150 155 160
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
165 170 175
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
180 185 190
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
195 200 205
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
210 215 220
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
225 230 235 240
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
245 250 255
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
260 265 270
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
275 280 285
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys
290 295 300
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
305 310 315 320
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
325 330 335
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
340 345 350
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
355 360 365
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
370 375 380
Lys Pro
385

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<210> 59
 <211> 1197
 <212> DNA
 <213> ospC Chimera

<220>
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 <222> (1)...(1197)

<400> 59
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480

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Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	
145																160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa															528	
Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	Thr	Asn	Gly	Thr	Lys			
															165	
170															175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca															576	
Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	
															180	
185															190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc															624	
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	
															195	
200															205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat															672	
Pro	Val	Val	Ala	Glu	Ser	Pro	Ala	Met	Val	Asn	Asn	Ser	Gly	Lys	Asp	
															210	
215															220	
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat															720	
Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	
															225	
230															235	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc															768	
Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	
															245	
250															255	
gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct															816	
Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala	
															260	
265															270	
aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag															864	
Lys	Ala	Ile	Gly	Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu		
															275	
280															285	
gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac															912	
Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	
															290	
295															300	
tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag															960	
Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	
															305	
310															315	
gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa															1008	
Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	
															325	
330															335	

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tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
 340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
 355 360 365

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
 370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

<210> 60
 <211> 399
 <212> PRT
 <213> ospC Chimera

<400> 60
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

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Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210 215 220
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225 230 235 240

 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245 250 255
 Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
 260 265 270
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
 275 280 285
 Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
 290 295 300
 Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
 305 310 315 320
 Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
 325 330 335
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
 340 345 350
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
 355 360 365
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
 370 375 380
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

<210> 61
 <211> 1196
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1196)

<400> 61
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

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 Concord, Massachusetts 01742-9133

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144		
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192		
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240		
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile			
65	70	75	80
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288		
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp			
85	90	95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336		
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384		
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu			
115	120	125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432		
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480		
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528		
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576		
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624		
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat	672		
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp			
210	215	220	

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ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225 230 235 240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg	768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245 250 255	
gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct	816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
260 265 270	
act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc	864
Thr Lys Ala Ile Gly Lys Ile Gln Gln Asn Gly Gly Leu Ala Val	
275 280 285	
gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca	912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
290 295 300	
aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta	960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu	
305 310 315 320	
aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa	1008
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys	
325 330 335	
aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat	1056
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp	
340 345 350	
gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag	1104
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys	
355 360 365	
ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca	1152
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala	
370 375 380	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac	1196
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu	
385 390 395	

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 Concord, Massachusetts 01742-9133

<210> 62
 <211> 398
 <212> PRT
 <213> ospC Chimera

<400> 62
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210 215 220
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225 230 235 240
 Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245 250 255
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
 260 265 270
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val
 275 280 285
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 290 295 300
 Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu
 305 310 315 320

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Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys
 325 330 335

Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp
 340 345 350
 Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys
 355 360 365
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala
 370 375 380
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390 395

<210> 63
 <211> 1185
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1185)

<400> 63
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt.aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta" gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser 100 105 110	336
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu 115 120 125	384
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr 130 135 140	432
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp 145 150 155 160	480
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp 165 170 175	528
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu 180 185 190	576
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr 195 200 205	624
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser 210 215 220	672
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile 225 230 235 240	720
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu 245 250 255	768
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly 260 265 270	816
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac	864

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Concord, Massachusetts 01742-9133

Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn			
275	280	285	
gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa			912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys			
290	295	300	
aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa			960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu			
305	310	315	320
aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa			1008
Lys Ala Lys Lys Cys Ser Gly Glu Phe Thr Ala Lys Leu Lys Gly Glu			
325	330	335	
cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa			1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys			
340	345	350	
gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt			1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu			
355	360	365	
gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag			1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu			
370	375	380	
atg ctt act aat tca gtt aaa gag ctt aca agc			1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser			
385	390	395	

<210> 64
 <211> 395
 <212> PRT
 <213> ospC Chimera

<400> 64
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

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 Concord, Massachusetts 01742-9133

Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160
 Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
 210 215 220
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
 225 230 235 240
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
 245 250 255
 Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly
 260 265 270
 Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
 275 280 285
 Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
 290 295 300
 Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
 305 310 315 320
 Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
 325 330 335
 His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
 340 345 350
 Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
 355 360 365
 Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
 370 375 380
 Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

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 Concord, Massachusetts 01742-9133

<210> 65
 <211> 1184
 <212> DNA
 <213> ospC Chimera

 <220>
 <221> CDS
 <222> (1) ... (1184)

 <400> 65
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

 gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

 gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110

 acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

 aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

 aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480

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 Concord, Massachusetts 01742-9133

Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat			528
Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta			576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu			
180	185	190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca			624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr			
195	200	205	
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct			672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser			
210	215	220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata			720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile			
225	230	235	240
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa			768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu			
245	250	255	
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att			816
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile			
260	265	270	
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat			864
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His			
275	280	285	
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca			912
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr			
290	295	300	
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att			960
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile			
305	310	315	320
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga			1008
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly			
325	330	335	

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gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa	1056		
Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys			
340	345		
350			
aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag	1104		
Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu			
355	360		
365			
ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa	1152		
Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys			
370	375		
380			
gag atg ctt gct aat tca gtt aaa gag ctt ac	1184		
Glu Met Leu Ala Asn Ser Val Lys Glu Leu			
385	390		
<210> 66			
<211> 394			
<212> PRT			
<213> ospC Chimera			
<400> 66			
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu			
65	70	75	80
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn			
85	90	95	
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser			
100	105	110	
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu			
115	120	125	
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr			
130	135	140	
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	

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Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
 210 215 220
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
 225 230 235 240
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
 245 250 255
 Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
 260 265 270
 Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His
 275 280 285
 Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr
 290 295 300
 Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile
 305 310 315 320
 Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly
 325 330 335
 Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys
 340 345 350
 Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu
 355 360 365
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys
 370 375 380
 Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390

<210> 67
 <211> 1184
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1184)

<400> 67
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 .	40
45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50	55
55	60
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu	
65	70
75	80
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn	
85	90
90	95
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100	105
105	110
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115	120
120	125
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130	135
135	140
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145	150
150	155
155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165	170
170	175
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180	185
185	190
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195	200
200	205

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agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser	
210 215 220	
aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt ctg gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	
gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att	816
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	
260 265 270	
ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac	864
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn	
275 280 285	
aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa	912
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu	
290 295 300	
aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca	960
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr	
305 310 315 320	
gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat	1008
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His	
325 330 335	
gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct	1056
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala	
340 345 350	
att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa	1104
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355 360 365	
aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr	
370 375 380	
tta aaa aat gct gtt aaa gag ctt aca agt cc	1184
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser	
385 390	

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<210> 68
 <211> 394
 <212> PRT
 <213> ospC Chimera

<400> 68
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser
 210 215 220
 Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
 225 230 235 240
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
 245 250 255
 Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
 260 265 270
 Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn
 275 280 285
 Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu
 290 295 300

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Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr
 305 310 315 320
 Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His
 325 330 335
 Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala
 340 345 350
 Ile Leu Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu
 355 360 365
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr
 370 375 380
 Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
 385 390

<210> 69
 <211> 1209
 <212> DNA
 <213> ospC Chimera

<220>
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 <222> (1)...(1209)

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336		
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser			
100	105	110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384		
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu			
115	120	125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432		
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr			
130	135	140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480		
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528		
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576		
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu			
180	185	190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624		
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr			
195	200	205	
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act	672		
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr			
210	215	220	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	720		
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys			
225	230	235	240
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	768		
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu			
245	250	255	
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa	816		
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys			
260	265	270	

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ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca	864		
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser			
275	280	285	
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta	912		
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu			
290	295	300	
agt gta ttg aat tca gaa gaa tta aag aaa att aaa gag gct aag	960		
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys			
305	310	315	320
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag	1008		
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu			
325	330	335	
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta	1056		
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu			
340	345	350	
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta	1104		
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu			
355	360	365	
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act	1152		
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr			
370	375	380	
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa	1200		
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys			
385	390	395	400
aaa cct taa	1209		
Lys Pro *			

<210> 70
 <211> 402
 <212> PRT
 <213> ospC Chimera

<400> 70
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

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 Concord, Massachusetts 01742-9133

Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
 210 215 220
 Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
 225 230 235 240
 Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
 245 250 255
 Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
 260 265 270
 Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
 275 280 285
 Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
 290 295 300
 Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys
 305 310 315 320
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
 325 330 335
 Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
 340 345 350
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
 355 360 365
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
 370 375 380
 Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
 385 390 395 400
 Lys Pro

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 Concord, Massachusetts 01742-9133

<210> 71
 <211> 1179
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1179)

<400> 71

atg	aga	tta	tta	ata	gga	ttt	gct	tta	gcg	tta	gct	tta	ata	gga	tgt	48
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys	
1		5						10					15			

gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	gga	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	
20				25							30					

gat	ggg	aat	gca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	144
Asp	Gly	Asn	Ala	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	
35				40					45							

aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	aca	gaa	tct	aac	gca	gtt	gtt	192
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	
50				55					60							

ctg	gcc	gtg	aaa	gaa	gtt	gag	acc	tta	ctt	gca	tct	ata	gat	gaa	ctt	240
Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Ala	Ser	Ile	Asp	Glu	Leu	
65				70					75				80			

gct	acc	aaa	gct	att	ggt	aaa	aaa	ata	ggc	aat	aat	ggt	tta	gag	gcc	288
Ala	Thr	Lys	Ala	Ile	Gly	Lys	Ile	Gly	Asn	Asn	Gly	Leu	Glu	Ala		
85				90					95							

aat	cag	agt	aaa	aac	aca	tca	ttg	tta	tca	gga	gct	tat	gca	ata	tct	336
Asn	Gln	Ser	Lys	Asn	Thr	Ser	Leu	Leu	Ser	Gly	Ala	Tyr	Ala	Ile	Ser	
100				105					110							

gac	cta	ata	gca	gaa	aaa	tta	aat	gta	ttg	aaa	aat	gaa	gaa	tta	aag	384
Asp	Leu	Ile	Ala	Glu	Lys	Leu	Asn	Val	Leu	Lys	Asn	Glu	Glu	Leu	Lys	
115				120					125							

gaa	aag	att	gat	aca	gct	aag	caa	tgt	tct	aca	gaa	ttt	act	aat	aaa	432
Glu	Lys	Ile	Asp	Thr	Ala	Lys	Gln	Cys	Ser	Thr	Glu	Phe	Thr	Asn	Lys	
130				135					140							

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ctt	aaa	agt	gaa	cat	gca	gtg	ctt	ggt	ctg	gac	aat	ctt	act	gat	gat	480	
Leu	Lys	Ser	Glu	His	Ala	Val	Leu	Gly	Leu	Asp	Asn	Leu	Thr	Asp	Asp		
145					150				155				160				
aat	gca	caa	aga	gct	att	tta	aaa	aaa	cat	gca	aat	aaa	gat	aag	ggt	528	
Asn	Ala	Gln	Arg	Ala	Ile	Leu	Lys	Lys	His	Ala	Asn	Lys	Asp	Lys	Gly		
					165				170			175					
gct	gca	gaa	ctt	gaa	aag	tta	ttt	aaa	gct	gta	gaa	aac	tta	tca	aaa	576	
Ala	Ala	Glu	Lys	Leu	Glu	Lys	Leu	Phe	Lys	Ala	Val	Glu	Asn	Leu	Ser	Lys	
					180				185			190					
gca	gct	caa	gac	aca	tta	aaa	aat	gct	gtt	aaa	gag	ctt	aca	agt	cct	624	
Ala	Ala	Gln	Asp	Thr	Leu	Lys	Asn	Ala	Val	Lys	Glu	Leu	Thr	Ser	Pro		
					195				200			205					
att	gtc	cat	ggt	aat	aat	tca	ggg	aaa	gat	ggg	aat	aca	tct	gca	aat	672	
Ile	Val	His	Gly	Asn	Asn	Ser	Gly	Lys	Asp	Gly	Asn	Thr	Ser	Ala	Asn		
					210				215			220					
tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	aat	ctt	aca	gaa	ata	agt	aaa	720	
Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys		
					225				230			235			240		
aaa	att	aca	gaa	tct	aac	gca	gtt	ctc	gcc	gtg	aaa	gaa	gtt	gaa		768	
Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu		
					245				250			255					
act	ttg	ctt	aca	tct	ata	gat	gag	ctt	gct	aaa	gct	att	ggt	aaa	aaa	816	
Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys		
					260				265			270					
ata	aaa	aac	gat	gtt	agt	tta	gat	aat	gag	gca	gat	cac	aac	gga	tca	864	
Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	Ser		
					275				280			285					
tta	ata	tca	gga	gca	tat	tta	att	tca	aac	tta	ata	aca	aaa	aaa	ata	912	
Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	Leu	Ile	Thr	Lys	Lys	Ile		
					290				295			300					
agt	gca	ata	aaa	gat	tca	gga	gaa	ttg	aag	gca	gaa	att	gaa	aag	gct	960	
Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala		
					305				310			315			320		
aag	aaa	tgt	tct	gaa	gaa	ttt	act	gct	aaa	tta	aaa	ggt	gaa	cac	aca	1008	
Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	Thr		
						325				330			335				

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gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att	1056
Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile	
340	345
350	
tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag	1104
Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys	
355	360
365	
tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt	1152
Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu	
370	375
380	
act aat tca gtt aaa gag ctt aca agc	1179
Thr Asn Ser Val Lys Glu Leu Thr Ser	
385	390
<210> 72	
<211> 393	
<212> PRT	
<213> ospC Chimera	
<400> 72	
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys	
1	5
10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20	25
30	
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35	40
45	
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	
50	55
60	
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu	
65	70
75	80
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala	
85	90
95	
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	
100	105
110	
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	
115	120
125	
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	
130	135
140	
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145	150
155	160
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly	
165	170
175	

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Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
 180 185 190
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
 210 215 220
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 225 230 235 240
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
 245 250 255
 Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys
 260 265 270
 Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser
 275 280 285
 Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile
 290 295 300
 Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala
 305 310 315 320
 Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr
 325 330 335

Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile
 340 345 350
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys
 355 360 365
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu
 370 375 380
 Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390

<210> 73
 <211> 1178
 <212> DNA
 <213> ospC Chimera

<220>
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 <222> (1)...(1178)

<400> 73
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

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gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa	96		
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144		
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt	192		
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val			
50	55	60	
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt	240		
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu			
65	70	75	80
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288		
Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala			
85	90	95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336		
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser			
100	105	110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384		
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys			
115	120	125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432		
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys			
130	135	140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480		
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp			
145	150	155	160
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528		
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly			
165	170	175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576		
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys			
180	185	190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624		
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro			
195	200	205	

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att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat	672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn	
210 215 220	
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt ctg gct gtg aaa gaa att gaa	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu	
245 250 255	
act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa	816
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys	
260 265 270	
aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga	864
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly	
275 280 285	
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys	
290 295 300	
tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn	
305 310 315 320	
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His	
325 330 335	
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala	
340 345 350	
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355 360 365	
aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met	
370 375 380	

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ctt gct aat tca gtt aaa gag ctt ac
 Leu Ala Asn Ser Val Lys Glu Leu
 385 390

1178

<210> 74
 <211> 392
 <212> PRT
 <213> ospC Chimera

<400> 74
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60
 Leu Ala Val Lys Glu Val Glu Thr Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
 165 170 175
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
 180 185 190
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
 210 215 220
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 225 230 235 240
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu
 245 250 255
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
 260 265 270

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Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly
 275 280 285
 Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys
 290 295 300
 Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn
 305 310 315 320
 Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His
 325 330 335
 Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala
 340 345 350
 Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu
 355 360 365
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met
 370 375 380
 Leu Ala Asn Ser Val Lys Glu Leu
 385 390

<210> 75
 <211> 1178
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1178)

<400> 75
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

 gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

 aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60

 ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80

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gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288		
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala			
85	90	95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336		
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser			
100	105	110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384		
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys			
115	120	125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432		
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys			
130	135	140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480		
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp			
145	150	155	160
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528		
Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly			
165	170	175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576		
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys			
180	185	190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624		
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro			
195	200	205	
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat	672		
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn			
210	215	220	
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720		
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys			
225	230	235	240
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag	768		
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu			
245	250	255	

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acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag	816	
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys		
260	265	
270		
aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca	864	
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser		
275	280	
285		
ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta	912	
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu		
290	295	
300		
aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag	960	
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys		
305	310	
315	320	
caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg	1008	
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val		
325	330	
335		
ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta	1056	
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu		
340	345	
350		
aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta	1104	
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu		
355	360	
365		
ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa	1152	
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys		
370	375	
380		
aat gct gtt aaa gag ctt aca agt cc	1178	
Asn Ala Val Lys Glu Leu Thr Ser		
385	390	
<210> 76		
<211> 392		
<212> PRT		
<213> ospC Chimera		
<400> 76		
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys		
1 5 10 15		
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys		
20 25 30		

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Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80

 Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
 165 170 175
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
 180 185 190
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn
 210 215 220
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 225 230 235 240
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
 245 250 255
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
 260 265 270
 Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser
 275 280 285
 Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu
 290 295 300
 Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
 305 310 315 320
 Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
 325 330 335
 Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
 340 345 350
 Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
 355 360 365
 Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
 370 375 380
 Asn Ala Val Lys Glu Leu Thr Ser
 385 390

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 Concord, Massachusetts 01742-9133

<210> 77
 <211> 1230
 <212> DNA
 <213> ospC Chimera

<220>
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<400> 77

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Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys
1		5					10						15		

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96

Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys
20				25						30					

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144

Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro
35					40					45					

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192

Asn	Leu	Thr	Glu	Ile	Ser	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	
50				55					60						

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240

Leu	Ala	Val	Lys	Glu	Val	Glu	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile
65				70			75			80					

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288

Ala	Ala	Lys	Ala	Ile	Gly	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp	
85					90				95						

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336

Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile
100				105						110					

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384

Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu
115				120					125						

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat			480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa			528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca			576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc			624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca			672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser			
210	215	220	
ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct			720
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro			
225	230	235	240
aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta			768
Asn Leu Thr Val Ile Ser Lys Ile Thr Asp Ser Asn Ala Phe Leu			
245	250	255	
ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt			816
Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu			
260	265	270	
tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac			864
Ser Lys Ala Ile Gly Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn			
275	280	285	
gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca			912
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser			
290	295	300	
aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag			960
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys			
305	310	315	320

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aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag	1008
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys	
325	330
335	
cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat	1056
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp	
340	345
350	
aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt	1104
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly	
355	360
365	
gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa	1152
Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys	
370	375
380	
gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct	1200
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro	
385	390
395	400
gtt gtg gca gaa agt cca aaa aaa cct taa	1230
Val Val Ala Glu Ser Pro Lys Lys Pro *	
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<212> PRT	
<213> ospC Chimera	
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys	
1	5
	10
	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20	25
	30
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35	40
	45
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50	55
	60
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65	70
	75
	80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85	90
	95
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100	105
	110
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115	120
	125

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser
 210 215 220
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro
 225 230 235 240
 Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu
 245 250 255
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 260 265 270
 Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn
 275 280 285
 Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser
 290 295 300
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys
 305 310 315 320
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys
 325 330 335
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp
 340 345 350
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly
 355 360 365
 Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys
 370 375 380
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro
 385 390 395 400
 Val Val Ala Glu Ser Pro Lys Lys Pro
 405

<210> 79
 <211> 1209
 <212> DNA
 <213> ospC Chimera

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 Concord, Massachusetts 01742-9133

<400> 79
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80

gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat 288
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95

acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata 336
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110

tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta 384
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125

aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat 432
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat 480
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160

gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa 528
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175

ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca 576

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 Concord, Massachusetts 01742-9133

Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser		
180	185	190
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624	
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser		
195	200	205
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca	672	
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser		
210	215	220
ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa	720	
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys		
225	230	235
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca	768	
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala		
245	250	255
gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat	816	
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp		
260	265	270
gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta	864	
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu		
275	280	285
gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta	912	
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu		
290	295	300
att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga	960	
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly		
305	310	315
gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt	1008	
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe		
325	330	335
act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt	1056	
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val		
340	345	350
act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa	1104	
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys		
355	360	365

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act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac	1152		
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn			
370	375		
380			
ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt	1200		
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu			
385	390		
395	400		
aca agc taa	1209		
Thr Ser *			
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<211> 402			
<212> PRT			
<213> ospC Chimera			
<400> 80			
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile			
65	70	75	80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp			
85	90	95	
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu			
115	120	125	
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser			
210	215	220	

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Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 225 230 235 240
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 245 250 255
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
 260 265 270
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
 275 280 285
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
 290 295 300
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
 305 310 315 320
 Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
 325 330 335
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
 340 345 350
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
 355 360 365
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
 370 375 380
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
 385 390 395 400
 Thr Ser

<210> 81
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<220>
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<400> 81
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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

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aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192		
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240		
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile			
65	70	75	80
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288		
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp			
85	90	95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336		
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384		
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu			
115	120	125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432		
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480		
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528		
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576		
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624		
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca	672		
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser			
210	215	220	
gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa	720		
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys			
225	230	235	240

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 Concord, Massachusetts 01742-9133

ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca	768	
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala		
245	250	255
gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat	816	
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp		
260	265	270
gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt	864	
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly		
275	280	285
tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat	912	
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr		
290	295	300
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca	960	
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser		
305	310	320
gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat	1008	
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp		
325	330	335
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat	1056	
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn		
340	345	350
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct	1104	
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala		
355	360	365
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa	1152	
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu		
370	375	380
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag	1200	
Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu		
385	390	395
ctt ac	1205	
Leu		

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 Concord, Massachusetts 01742-9133

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 <213> ospC Chimera

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 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
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 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
 210 215 220
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 225 230 235 240
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala
 245 250 255
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp
 260 265 270
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly
 275 280 285
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr
 290 295 300
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser
 305 310 315 320

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Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
 325 330 335
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
 340 345 350
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
 355 360 365
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
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 Asn Leu Ala Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
 385 390 395 400
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<220>
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<400> 83

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														15		
gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	agt	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Ser	Asn	Ser	Gly	Lys	
20															30	
ggg	ggg	gat	tct	gca	tct	act	aat	cct	gct	gac	gag	tct	gct	aaa	ggg	144
Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Ala	Asp	Glu	Ser	Ala	Lys	Gly	
35															45	
cct	aat	ctt	aca	gaa	ata	agc	aaa	aaa	att	aca	gat	tct	aat	gca	ttt	192
Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	
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gta	ctt	gct	gtt	aaa	gaa	gtt	gag	act	ttg	gtt	tta	tct	ata	gat	gaa	240
Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Val	Leu	Ser	Ile	Asp	Glu	
65															80	
ctt	gct	aag	aaa	gct	att	ggt	caa	aaa	ata	gac	aat	aat	aat	ggt	tta	288
Leu	Ala	Lys	Lys	Ala	Ile	Gly	Gln	Lys	Ile	Asp	Asn	Asn	Asn	Gly	Leu	
85															95	

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gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca	336
Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala	
100	105
110	
ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa	384
Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu	
115	120
125	
gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt	432
Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe	
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140	
act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct	480
Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala	
145	150
155	160
acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc	528
Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr	
165	170
175	
gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt	576
Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly	
180	185
190	
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Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu	
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Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn	
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235	240
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260	265
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gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta	864
Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu	
275	280
285	

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gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa	912		
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315	320		
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Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr			
325	330		
335			
act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag	1056		
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln			
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gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac	1104		
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp			
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370	375		
380			
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385	390		
395	400		
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Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly			
35	40	45	

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Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 50 55 60
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
 65 70 75 80
 Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
 85 90 95
 Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala
 100 105 110
 Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu
 115 120 125
 Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe
 130 135 140
 Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala
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 Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr
 165 170 175
 Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly
 180 185 190
 Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu
 195 200 205
 Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn
 210 215 220
 Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys
 225 230 235 240
 Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala
 245 250 255
 Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp
 260 265 270
 Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu
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 Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu
 290 295 300
 Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu
 305 310 315 320
 Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr
 325 330 335
 Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln
 340 345 350
 Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp
 355 360 365
 Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu
 370 375 380
 Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
 385 390 395 400
 Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 405 410

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<210> 85
<211> 192
<212> PRT
<213> borrelia burgdorferi

<400> 85

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					20			25					30		
Glu	Ser	Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu
					35			40				45			
Thr	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Lys	Asn
					50			55			60				
Asp	Val	Ser	Leu	Asp	Asn	Glu	Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser
					65			70			75		80		
Gly	Ala	Tyr	Leu	Ile	Ser	Thr	Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile
					85			90			95				
Lys	Asp	Ser	Gly	Glu	Leu	Lys	Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys
					100			105			110				
Ser	Glu	Glu	Phe	Thr	Ala	Lys	Leu	Lys	Gly	Glu	His	Thr	Asp	Leu	Gly
					115			120			125				
Lys	Glu	Gly	Val	Thr	Asp	Asp	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Lys	Thr
					130			135			140				
Asn	Asn	Asp	Lys	Thr	Lys	Gly	Ala	Asp	Glu	Leu	Glu	Lys	Leu	Phe	Glu
					145			150			155		160		
Ser	Val	Lys	Asn	Leu	Ser	Lys	Ala	Ala	Lys	Glu	Met	Leu	Thr	Asn	Ser
					165			170			175				
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<210> 86
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<213> borrelia burgdorferi

<400> 86

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					20			25			30				
Asn	Ala	Val	Val	Leu	Ala	Val	Lys	Glu	Ile	Glu	Thr	Leu	Ala	Ser	
					35			40			45				

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Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Lys	Ile	Gln	Gln	Asn
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Gly	Gly	Leu	Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly
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Ala	Tyr	Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys
									85		90			95	
Asn	Ser	Glu	Lys	Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser
								100		105				110	
Glu	Asp	Phe	Thr	Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile
								115		120			125		
Glu	Asn	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp
								130		135			140		
Ala	Ala	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala
145								150			155				160
Val	Glu	Asn	Leu	Ala	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val
								165			170			175	
Lys	Glu	Leu	Thr	Ser	Pro	Ile	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	
								180			185			190	

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UNITED STATES PATENT AND TRADEMARK OFFICE
CERTIFICATE OF CORRECTION

PATENT NO. : 7,060,281 B1

DATED : June 13, 2006

INVENTOR(S) : Raymond J. Dattwyler, Gerald Seinost, Daniel
Dykhuizen, Benjamin J. Luft, Maria J.C. Gomes-Solecki

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

At Column 45, Insert SEQ ID NOS. 53-86 after SEQ ID NO: 52

<210> 53

<211> 1137

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1137)

<400> 53

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Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
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att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg	144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	

ttg ctg tca tct ata gat gag ctt gct aaa gct att ggt aaa aaa ata	192
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Lys	Asn	Asp	Gly	Ser	Leu	Asp	Asn	Glu	Ala	Asn	Arg	Asn	Glu	Ser	Leu	
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tta	gca	gga	gct	tat	aca	ata	tca	acc	tta	ata	aca	caa	aaa	tta	agt	288
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Lys	Leu	Asn	Gly	Ser	Glu	Gly	Leu	Lys	Glu	Lys	Ile	Ala	Ala	Ala	Lys	
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Ser	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	Asp	Glu	Ser	Ala	Lys	Gly	
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Pro	Asn	Leu	Thr	Val	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Phe	
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Leu	Leu	Ala	Val	Lys	Glu	Val	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu		
225					230					235			240			

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ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat	768
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255	
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270	
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315	320
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 50 55 60
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 145 150 155 160
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 165 170 175
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 195 200 205
 Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 210 215 220
 Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu
 225 230 235 240
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 245 250 255
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 260 265 270
 Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu
 275 280 285
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 290 295 300
 Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp
 305 310 315 320

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Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser			
1	5	10	15
gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa aaa			96
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys			
20	25	30	
att acg gat tct aat gcg gtt tta ctt gct gtg aaa gag gtt gaa gcg			144
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala			
35	40	45	
ttg ctg tca tct ata gat gaa att gct gct aaa gct att ggt aaa aaa			192
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys			
50	55	60	
ata cac caa aat aat ggt ttg gat acc gaa tat aat cac aat gga tca			240
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser			
65	70	75	80
ttg tta gcg gga gct tat gca ata tca acc cta ata aaa caa aaa tta			288
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu			
85	90	95	

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gat gga ttg aaa aat gaa gga tta aag gaa aaa att gat gcg gct aag	336
Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys	
100	105
110	
aaa tgt tct gaa aca ttt act aat aaa tta aaa gaa aaa cac aca gat	384
Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp	
115	120
125	
ctt ggt aaa gaa ggt gtt act gat gct gat gca aaa gaa gcc att tta	432
Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu	
130	135
140	
aaa aca aat ggt act aaa act aaa ggt gct gaa gaa ctt gga aaa tta	480
Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu	
145	150
155	160
ttt gaa tca gta gag gtc ttg tca aaa gca gct aaa gag atg ctt gct	528
Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala	
165	170
175	
aat tca gtt aaa gag ctt aca agc cct gtt gtg gca gaa agt cca aaa	576
Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys	
180	185
190	
aaa cct ttc cat ggt aat aat tca ggt ggg gat tct gca tct act aat	624
Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn	
195	200
205	
cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa aaa	672
Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys	
210	215
220	
att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag gct	720
Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala	
225	230
235	240
ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa ata	768
Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile	
245	250
255	
aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca ttg	816
Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu	
260	265
270	
ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta agt	864
Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser	
275	280
285	

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gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag gat	912
Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp	
290	295
305	310
325	330
340	345
355	360
370	375
385	
<210> 56	
<211> 385	
<212> PRT	
<213> ospC Chimera	
<400> 56	
Met Ala Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser	
1 5 10 15	
Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20 25 30	
Ile Thr Asp Ser Asn Ala Val Leu Leu Ala Val Lys Glu Val Glu Ala	
35 40 45	
Leu Leu Ser Ser Ile Asp Glu Ile Ala Ala Lys Ala Ile Gly Lys Lys	
50 55 60	
Ile His Gln Asn Asn Gly Leu Asp Thr Glu Tyr Asn His Asn Gly Ser	
65 70 75 80	

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Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Lys Gln Lys Leu
 85 90 95
 Asp Gly Leu Lys Asn Glu Gly Leu Lys Glu Lys Ile Asp Ala Ala Lys
 100 105 110
 Lys Cys Ser Glu Thr Phe Thr Asn Lys Leu Lys Glu Lys His Thr Asp
 115 120 125
 Leu Gly Lys Glu Gly Val Thr Asp Ala Asp Ala Lys Glu Ala Ile Leu
 130 135 140
 Lys Thr Asn Gly Thr Lys Thr Lys Gly Ala Glu Glu Leu Gly Lys Leu
 145 150 155 160
 Phe Glu Ser Val Glu Val Leu Ser Lys Ala Ala Lys Glu Met Leu Ala
 165 170 175
 Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys
 180 185 190
 Lys Pro Phe His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn
 195 200 205
 Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys Lys
 210 215 220
 Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu Ala
 225 230 235 240
 Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile
 245 250 255
 Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu
 260 265 270
 Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser
 275 280 285
 Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys Asp
 290 295 300
 Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu Leu
 305 310 315 320
 Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys
 325 330 335
 Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu Phe
 340 345 350
 Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn
 355 360 365
 Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys Lys
 370 375 380

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Pro
385

<210> 57
 <211> 1161
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1161)

<400> 57

atg	tgt	agt	aat	tca	ggg	aaa	ggt	ggg	gat	tct	gca	tct	act	aat	cct	48
Met	Cys	Ser	Asn	Ser	Gly	Lys	Gly	Gly	Asp	Ser	Ala	Ser	Thr	Asn	Pro	
1				5					10				15			

gct gac gag tct gcg aaa ggg cct aat ctt aca gaa ata agc aaa aaa 96

Ala	Asp	Glu	Ser	Ala	Lys	Gly	Pro	Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	
					20				25				30			

att aca gat tct aat gca ttt gta ctt gct gtt aaa gaa gtt gag act 144

Ile	Thr	Asp	Ser	Asn	Ala	Phe	Val	Leu	Ala	Val	Lys	Glu	Val	Glu	Thr	
					35			40				45				

ttg gtt tta tct ata gat gaa ctt gct aag aaa gct att ggt caa aaa 192

Leu	Val	Leu	Ser	Ile	Asp	Glu	Leu	Ala	Lys	Lys	Ala	Ile	Gly	Gln	Lys	
					50			55			60					

ata gac aat aat aat ggt tta gct gct tta aat aat cag aat gga tcg 240

Ile	Asp	Asn	Asn	Gly	Leu	Ala	Ala	Leu	Asn	Asn	Gln	Asn	Gly	Ser	
					65			70			75		80		

ttg tta gca gga gcc tat gca ata tca acc cta ata aca gaa aaa ttg 288

Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	Ser	Thr	Leu	Ile	Thr	Glu	Lys	Leu	
					85			90			95					

agt aaa ttg aaa aat tta gaa gaa tta aag aca gaa att gca aag gct 336

Ser	Lys	Leu	Lys	Asn	Leu	Glu	Lys	Thr	Glu	Ile	Ala	Lys	Ala		
					100			105			110				

aag aaa tgt tcc gaa gaa ttt act aat aaa cta aaa agt ggt cat gca 384

Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Asn	Lys	Leu	Lys	Ser	Gly	His	Ala	
					115			120			125					

gat ctt ggc aaa cag gat gct acc gat gat cat gca aaa gca gct att 432

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Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile			
130	135	140	
tta aaa aca cat gca act acc gat aaa ggt gct aaa gaa ttt aaa gat			480
Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp			
145	150	155	160
tta ttt gaa tca gta gaa ggt ttg tta aaa gca gct caa gta gca cta			528
Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu			
165	170	175	
act aat tca gtt aaa gaa ctt aca agt cct gtt gta gca gaa agt cca			576
Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro			
180	185	190	
aaa aaa cct cat atg gct aat aat tca ggt ggg gat tct gca tct act			624
Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr			
195	200	205	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa			672
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys			
210	215	220	
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag			720
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu			
225	230	235	240
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa			768
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys			
245	250	255	
ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca			816
Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser			
260	265	270	
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta			864
Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu			
275	280	285	
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag			912
Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Lys Ile Lys Glu Ala Lys			
290	295	300	
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag			960
Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu			
305	310	315	320

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ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta	1008
Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu	
325	330
335	
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta	1056
Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu	
340	345
350	
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act	1104
Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr	
355	360
365	
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa	1152
Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys	
370	375
380	
aaa cct taa	1161
Lys Pro *	
385	
<210> 58	
<211> 386	
<212> PRT	
<213> ospC Chimera	
<400> 58	
Met Cys Ser Asn Ser Gly Lys Gly Gly Asp Ser Ala Ser Thr Asn Pro	
1	5
	10
	15
Ala Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys	
20	25
	30
Ile Thr Asp Ser Asn Ala Phe Val Leu Ala Val Lys Glu Val Glu Thr	
35	40
	45
Leu Val Leu Ser Ile Asp Glu Leu Ala Lys Lys Ala Ile Gly Gln Lys	
50	55
	60
Ile Asp Asn Asn Asn Gly Leu Ala Ala Leu Asn Asn Gln Asn Gly Ser	
65	70
	75
	80
Leu Leu Ala Gly Ala Tyr Ala Ile Ser Thr Leu Ile Thr Glu Lys Leu	
85	90
	95
Ser Lys Leu Lys Asn Leu Glu Leu Lys Thr Glu Ile Ala Lys Ala	
100	105
	110
Lys Lys Cys Ser Glu Glu Phe Thr Asn Lys Leu Lys Ser Gly His Ala	
115	120
	125
Asp Leu Gly Lys Gln Asp Ala Thr Asp Asp His Ala Lys Ala Ala Ile	
130	135
	140

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Leu Lys Thr His Ala Thr Thr Asp Lys Gly Ala Lys Glu Phe Lys Asp
 145 150 155 160
 Leu Phe Glu Ser Val Glu Gly Leu Leu Lys Ala Ala Gln Val Ala Leu
 165 170 175
 Thr Asn Ser Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro
 180 185 190
 Lys Lys Pro His Met Ala Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
 195 200 205
 Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
 210 215 220
 Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
 225 230 235 240
 Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
 245 250 255
 Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
 260 265 270
 Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
 275 280 285
 Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys
 290 295 300
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
 305 310 315 320
 Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
 325 330 335
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
 340 345 350
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
 355 360 365
 Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
 370 375 380
 Lys Pro
 385

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<210> 59
 <211> 1197

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1197)

<400> 59

atg	aga	tta	tta	ata	gga	ttt	gct	tta	gct	tta	ata	gga	tgt	48	
Met	Arg	Leu	Ieu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys
1															15

gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	
															20	
															30	

gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	144
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	
															35	
															40	
															45	

aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	acg	gat	tct	aat	gct	ggg	ttt	192
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	
															50	
															55	
															60	

ctt	gct	gtg	aaa	gag	gtt	gaa	gct	ttg	ctg	tca	tct	ata	gat	gaa	att	240
Leu	Ala	Val	Lys	Glu	Val	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile		
															65	
															70	
															75	
															80	

gct	gct	aaa	gct	att	ggt	aaa	aaa	ata	cac	caa	aat	aat	ggt	ttg	gat	288
Ala	Ala	Lys	Ala	Ile	Gly	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp		
															85	
															90	
															95	

acc	gaa	tat	aat	cac	aat	gga	tca	ttg	tta	gct	ttt	act	aat	336	
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ile	
															100
															105
															110

tca	acc	cta	ata	aaa	caa	aaa	tta	gat	gga	ttg	aaa	aat	gaa	gga	tta	384
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Asn	Glu	Gly	Leu		
															115	
															120	
															125	

aag	gaa	aaa	att	gat	gct	aag	aaa	tgt	tct	gaa	aca	ttt	act	aat	432
Lys	Glu	Lys	Ile	Asp	Ala	Ala	Lys	Lys	Cys	Ser	Glu	Thr	Phe	Thr	Asn
															130
															135
															140

aaa	tta	aaa	gaa	aaa	cac	aca	gat	ctt	ggt	aaa	gaa	ggg	tgt	act	gat	480
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Lys	Leu	Lys	Glu	Lys	His	Thr	Asp	Leu	Gly	Lys	Glu	Gly	Val	Thr	Asp	
145																160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa															528	
Ala	Asp	Ala	Lys	Glu	Ala	Ile	Leu	Lys	Thr	Asn	Gly	Thr	Lys			
															165	
170															175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca															576	
Gly	Ala	Glu	Glu	Leu	Gly	Lys	Leu	Phe	Glu	Ser	Val	Glu	Val	Leu	Ser	
															180	
185															190	
aaa gca gct,aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc															624	
Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val	Lys	Glu	Leu	Thr	Ser	
															195	
200															205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca ggg aaa gat															672	
Pro	Val	Val	Ala	Glu	Ser	Pro	Ala	Met	Val	Asn	Asn	Ser	Gly	Lys	Asp	
															210	
215															220	
ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat															720	
Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	Asn	
															225	
230															235	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctc															768	
Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Glu	Ser	Asn	Ala	Val	Val	Leu	
															245	
250															255	
gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat gag ctt gct															816	
Ala	Val	Lys	Glu	Val	Glu	Thr	Leu	Leu	Thr	Ser	Ile	Asp	Glu	Leu	Ala	
															260	
265															270	
aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta gat aat gag															864	
Lys	Ala	Ile	Gly	Lys	Ile	Lys	Asn	Asp	Val	Ser	Leu	Asp	Asn	Glu		
															275	
280															285	
gca gat cac aac gga tca tta ata tca gga gca tat tta att tca aac															912	
Ala	Asp	His	Asn	Gly	Ser	Leu	Ile	Ser	Gly	Ala	Tyr	Leu	Ile	Ser	Asn	
															290	
295															300	
tta ata aca aaa aaa ata agt gca ata aaa gat tca gga gaa ttg aag															960	
Leu	Ile	Thr	Lys	Lys	Ile	Ser	Ala	Ile	Lys	Asp	Ser	Gly	Glu	Leu	Lys	
															305	
310															315	
gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt act gct aaa															1008	
Ala	Glu	Ile	Glu	Lys	Ala	Lys	Lys	Cys	Ser	Glu	Glu	Phe	Thr	Ala	Lys	
															325	
330															335	

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tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt act gat gat 1056
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
 340 345 350

aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa act aag ggc 1104
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
 355 360 365

gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa 1152
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
 370 375 380

gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt aca agc 1197
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

<210> 60
 <211> 399
 <212> PRT
 <213> ospC Chimera

<400> 60
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190

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Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210 215 220
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225 230 235 240

 Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245 250 255
 Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala
 260 265 270
 Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu
 275 280 285
 Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn
 290 295 300
 Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys
 305 310 315 320
 Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys
 325 330 335
 Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp
 340 345 350
 Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly
 355 360 365
 Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys
 370 375 380
 Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

<210> 61
 <211> 1196
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1196)

<400> 61
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144		
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192		
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240		
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile			
65	70	75	80
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288		
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp			
85	90	95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336		
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384		
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu			
115	120	125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432		
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480		
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528		
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576		
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624		
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca gcc atg gta aat aat tca gga aaa gat	672		
Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp			
210	215	220	

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ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct aat	720
Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn	
225 230 235 240	
ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt ctg	768
Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu	
245 250 255	
gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat gaa ctt gct	816
Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala	
260 265 270	
act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc	864
Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val	
275 280 285	
gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat aca ata tca	912
Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
290 295 300	
aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca gaa aaa tta	960
Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu	
305 310 315 320	
aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat ttt act aaa	1008
Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys	
325 330 335	
aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat gtt act gat	1056
Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp	
340 345 350	
gag aat gca aaa aaa gct att tta ata aca gat gca gct aaa gat aag	1104
Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys	
355 360 365	
ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca	1152
Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala	
370 375 380	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt ac	1196
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu	
385 390 395	

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<210> 62

<211> 398

<212> PRT

<213> ospC Chimera

<400> 62

Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Ala Met Val Asn Asn Ser Gly Lys Asp
 210 215 220
 Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn
 225 230 235 240
 Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val Leu
 245 250 255
 Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala
 260 265 270
 Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val
 275 280 285
 Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 290 295 300
 Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu
 305 310 315 320

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Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys
 325 330 335

Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp
 340 345 350
 Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys
 355 360 365
 Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala
 370 375 380
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390 395

<210> 63

<211> 1185

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1185)

<400> 63

atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336		
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser			
100	105	110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384		
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu			
115	120	125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432		
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr			
130	135	140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480		
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528		
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576		
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu			
180	185	190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624		
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr			
195	200	205	
agc cct gtt gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct	672		
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser			
210	215	220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720		
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile			
225	230	235	240
agt aaa aaa att aca gaa tct aac gca gtt gtt ctc gcc gtg aaa gaa	768		
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu			
245	250	255	
gtt gaa act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt	816		
Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly			
260	265	270	
aaa aaa ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac	864		
	7,060,281 B1		

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Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn			
275	280	285	
gga tca tta ata tca gga gca tat tta att tca aac tta ata aca aaa			912
Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys			
290	295	300	
aaa ata agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa			960
Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu			
305	310	315	320
aag gct aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa			1008
Lys Ala Lys Lys Cys Ser Gly Glu Phe Thr Ala Lys Leu Lys Gly Glu			
325	330	335	
cac aca gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa			1056
His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys			
340	345	350	
gcc att tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt			1104
Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu			
355	360	365	
gaa aag tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag			1152
Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu			
370	375	380	
atg ctt act aat tca gtt aaa gag ctt aca agc			1185
Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser			
385	390	395	

<210> 64
 <211> 395
 <212> PRT
 <213> ospC Chimera

<400> 64
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

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Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175
 Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
 210 215 220
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
 225 230 235 240
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
 245 250 255
 Val Glu Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly
 260 265 270
 Lys Lys Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn
 275 280 285
 Gly Ser Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys
 290 295 300
 Lys Ile Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu
 305 310 315 320
 Lys Ala Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu
 325 330 335
 His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys
 340 345 350
 Ala Ile Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu
 355 360 365
 Glu Lys Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu
 370 375 380
 Met Leu Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390 395

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<210> 65
 <211> 1184

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1184)

<400> 65

atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca 336
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110

acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta 384
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125

aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act 432
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat 480

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Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat			528
Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta			576
Lys Gly Val Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu			
180	185	190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca			624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr			
195	200	205	
agc cct gtt gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct			672
Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser			
210	215	220	
gca aat tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata			720
Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile			
225	230	235	240
agt aaa aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa			768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu			
245	250	255	
att gaa act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att			816
Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile			
260	265	270	
ggt aaa aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat			864
Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His			
275	280	285	
aat gga aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca			912
Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr			
290	295	300	
caa aaa tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att			960
Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile			
305	310	315	320
gaa aat gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga			1008
Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly			
325	330	335	

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gaa cat gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa 1056
 Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys
 340 345 350

aaa gct att tta ata aca gat gca gct aaa gat aag ggc gct gca gag 1104
 Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu
 355 360 365

ctt gaa aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa 1152
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys
 370 375 380

gag atg ctt gct aat tca gtt aaa gag ctt ac 1184
 Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390

<210> 66
 <211> 394
 <212> PRT
 <213> ospC Chimera

<400> 66
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175

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Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser
 210 215 220
 Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
 225 230 235 240
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
 245 250 255
 Ile Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
 260 265 270
 Gly Lys Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His
 275 280 285
 Asn Gly Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr
 290 295 300
 Gln Lys Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile
 305 310 315 320
 Glu Asn Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly
 325 330 335
 Glu His Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys
 340 345 350
 Lys Ala Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu
 355 360 365
 Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys
 370 375 380
 Glu Met Leu Ala Asn Ser Val Lys Glu Leu
 385 390

<210> 67
 <211> 1184
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1184)

<400> 67
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

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gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144		
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192		
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt	240		
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu			
65	70	75	80
gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat	288		
Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn			
85	90	95	
gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336		
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser			
100	105	110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384		
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu			
115	120	125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432		
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr			
130	135	140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480		
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp			
145	150	155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528		
Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp			
165	170	175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576		
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu			
180	185	190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624		
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr			
195	200	205	

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agc cct gtt gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct	672
Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser	
210 215 220	
aca aat tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata	720
Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile	
225 230 235 240	
agt aaa aaa att aca gaa tct aac gca gtt ctg gcc gtg aaa gaa	768
Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu	
245 250 255	
gtt gag acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att	816
Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile	
260 265 270	
ggt aag aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac	864
Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn	
275 280 285	
aca tca ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa	912
Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu	
290 295 300	
aaa tta aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca	960
Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr	
305 310 315 320	
gct aag caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat	1008
Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His	
325 330 335	
gca gtg ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct	1056
Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala	
340 345 350	
att tta aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa	1104
Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu	
355 360 365	
aag tta ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca	1152
Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr	
370 375 380	
tta aaa aat gct gtt aaa gag ctt aca agt cc	1184
Leu Lys Asn Ala Val Lys Glu Leu Thr Ser	
385 390	

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<210> 68
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 <212> PRT
 <213> ospC Chimera

<400> 68
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 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140

 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser
 210 215 220
 Thr Asn Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile
 225 230 235 240
 Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu
 245 250 255
 Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile
 260 265 270
 Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn
 275 280 285
 Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu
 290 295 300

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Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr
 305 310 315 320
 Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His
 325 330 335
 Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala
 340 345 350
 Ile Leu Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu
 355 360 365
 Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr
 370 375 380
 Leu Lys Asn Ala Val Lys Glu Leu Thr Ser
 385 390

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 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

 aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta 192
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60

 ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gag ctt 240
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80

 gct aaa gct att ggt aaa aaa ata aaa aac gat ggt agt tta gat aat 288
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95

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gaa gca aat cgc aac gag tca ttg tta gca gga gct tat aca ata tca	336
Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser	
100	105
110	
acc tta ata aca caa aaa tta agt aaa tta aac gga tca gaa ggt tta	384
Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu	
115	120
125	
aag gaa aag att gcc gca gct aag aaa tgc tct gaa gag ttt agt act	432
Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr	
130	135
140	
aaa cta aaa gat aat cat gca cag ctt ggt ata cag ggc gtt act gat	480
Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp	
145	150
155	160
gaa aat gca aaa aaa gct att tta aaa gca aat gca gcg ggt aaa gat	528
Glu Asn Ala Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp	
165	170
175	
aag ggc gtt gaa gaa ctt gaa aag ttg tcc gga tca tta gaa agc tta	576
Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu	
180	185
190	
tca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca	624
Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr	
195	200
205	
agc cct gtt gtc cat ggt aat aat tca ggt ggg gat tct gca tct act	672
Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr	
210	215
220	
aat cct gat gag tct gca aaa gga cct aat ctt acc gta ata agc aaa	720
Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys	
225	230
235	240
aaa att aca gat tct aat gca ttt tta ctg gct gtg aaa gaa gtt gag	768
Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu	
245	250
255	
gct ttg ctt tca tct ata gat gaa ctt tct aaa gct att ggt aaa aaa	816
Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys	
260	265
270	

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ata aaa aat gat ggt act tta gat aac gaa gca aat cga aac gaa tca Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser 275 280 285	864		
ttg ata gca gga gct tat gaa ata tca aaa cta ata aca caa aaa tta Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu 290 295 300	912		
agt gta ttg aat tca gaa gaa tta aag aaa aaa att aaa gag gct aag Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys 305 310 315 320	960		
gat tgt tcc caa aaa ttt act act aag cta aaa gat agt cat gca gag Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu 325 330 335	1008		
ctt ggt ata caa agc gtt cag gat gat aat gca aaa aaa gct att tta Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu 340 345 350	1056		
aaa aca cat gga act aaa gac aag ggt gct aaa gaa ctt gaa gag tta Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu 355 360 365	1104		
ttt aaa tca cta gaa agc ttg tca aaa gca gcg caa gca gca tta act Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr 370 375 380	1152		
aat tca gtt aaa gag ctt aca aat cct gtt gtg gca gaa agt cca aaa Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys 385 390 395 400	1200		
aaa cct taa Lys Pro *	1209		
<210> 70			
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<212> PRT			
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	

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Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Ser Leu Asp Asn
 85 90 95
 Glu Ala Asn Arg Asn Glu Ser Leu Leu Ala Gly Ala Tyr Thr Ile Ser
 100 105 110
 Thr Leu Ile Thr Gln Lys Leu Ser Lys Leu Asn Gly Ser Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Ala Ala Lys Lys Cys Ser Glu Glu Phe Ser Thr
 130 135 140
 Lys Leu Lys Asp Asn His Ala Gln Leu Gly Ile Gln Gly Val Thr Asp
 145 150 155 160
 Glu Asn Ala Lys Lys Ala Ile Leu Lys Ala Asn Ala Ala Gly Lys Asp
 165 170 175
 Lys Gly Val Glu Glu Leu Glu Lys Leu Ser Gly Ser Leu Glu Ser Leu
 180 185 190
 Ser Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr
 195 200 205
 Ser Pro Val Val His Gly Asn Asn Ser Gly Gly Asp Ser Ala Ser Thr
 210 215 220
 Asn Pro Asp Glu Ser Ala Lys Gly Pro Asn Leu Thr Val Ile Ser Lys
 225 230 235 240
 Lys Ile Thr Asp Ser Asn Ala Phe Leu Leu Ala Val Lys Glu Val Glu
 245 250 255
 Ala Leu Leu Ser Ser Ile Asp Glu Leu Ser Lys Ala Ile Gly Lys Lys
 260 265 270
 Ile Lys Asn Asp Gly Thr Leu Asp Asn Glu Ala Asn Arg Asn Glu Ser
 275 280 285
 Leu Ile Ala Gly Ala Tyr Glu Ile Ser Lys Leu Ile Thr Gln Lys Leu
 290 295 300
 Ser Val Leu Asn Ser Glu Glu Leu Lys Lys Ile Lys Glu Ala Lys
 305 310 315 320
 Asp Cys Ser Gln Lys Phe Thr Thr Lys Leu Lys Asp Ser His Ala Glu
 325 330 335
 Leu Gly Ile Gln Ser Val Gln Asp Asp Asn Ala Lys Lys Ala Ile Leu
 340 345 350
 Lys Thr His Gly Thr Lys Asp Lys Gly Ala Lys Glu Leu Glu Glu Leu
 355 360 365
 Phe Lys Ser Leu Glu Ser Leu Ser Lys Ala Ala Gln Ala Ala Leu Thr
 370 375 380
 Asn Ser Val Lys Glu Leu Thr Asn Pro Val Val Ala Glu Ser Pro Lys
 385 390 395 400
 Lys Pro

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621605
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Concord, Massachusetts 01742-9133

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<210> 71
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1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
65 70 75 80

gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc 288
Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
85 90 95

aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct 336
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
100 105 110

gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag 384
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
115 120 125

gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa 432
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
130 135 140

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ctt aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528
Asn Ala Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys Gly	
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	
195 200 205	
att gtc cat ggt aat aat tca ggg aaa gat ggg aat aca tct gca aat	672
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn	
210 215 220	
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys	
225 230 235 240	
aaa att aca gaa tct aac gca gtt ctt ctc gcc gtg aaa gaa gtt gaa	768
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu	
245 250 255	
act ttg ctt aca tct ata gat gag ctt gct aaa gct att ggt aaa aaa	816
Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys	
260 265 270	
ata aaa aac gat gtt agt tta gat aat gag gca gat cac aac gga tca	864
Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser	
275 280 285	
tta ata tca gga gca tat tta att tca aac tta ata aca aaa aaa ata	912
Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile	
290 295 300	
agt gca ata aaa gat tca gga gaa ttg aag gca gaa att gaa aag gct	960
Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala	
305 310 315 320	
aag aaa tgt tct gaa gaa ttt act gct aaa tta aaa ggt gaa cac aca	1008
Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr	
325 330 335	

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gat ctt ggt aaa gaa ggc gtt act gat gat aat gca aaa aaa gcc att 1056
 Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile
 340 345 350

tta aaa aca aat aat gat aaa act aag ggc gct gat gaa ctt gaa aag 1104
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys
 355 360 365

tta ttt gaa tca gta aaa aac ttg tca aaa gca gct aaa gag atg ctt 1152
 Leu Phe Glu Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu
 370 375 380

act aat tca gtt aaa gag ctt aca agc 1179
 Thr Asn Ser Val Lys Glu Leu Thr Ser
 385 390

<210> 72
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 <212> PRT
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<400> 72
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 20 25 30
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
 165 170 175

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Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
 180 185 190
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
 210 215 220
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 225 230 235 240
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
 245 250 255
 Thr Leu Leu Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys
 260 265 270
 Ile Lys Asn Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser
 275 280 285
 Leu Ile Ser Gly Ala Tyr Leu Ile Ser Asn Leu Ile Thr Lys Lys Ile
 290 295 300
 Ser Ala Ile Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala
 305 310 315 320
 Lys Lys Cys Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr
 325 330 335

Asp Leu Gly Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile
 340 345 350
 Leu Lys Thr Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys
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 1 5 10 15

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gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	144
35 40 45	
aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val	192
50 55 60	
ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu	240
65 70 75 80	
gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala	288
85 90 95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser	336
100 105 110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys	384
115 120 125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys	432
130 135 140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp	480
145 150 155 160	
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt Asn Ala Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys Gly	528
165 170 175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys	576
180 185 190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro	624
195 200 205	

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att gtc cat ggt aat aat tca gga aaa gat ggg aat aca tct gca aat	672																																																																																		
Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn																																																																																			
210	215	220		tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720	Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys		225	230	235	240	aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa	768	Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu		245	250	255		act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa	816	Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys		260	265	270		aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga	864	Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly		275	280	285		aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912	Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys		290	295	300		tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960	Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn		305	310	315	320	gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008	Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His		325	330	335		gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056	Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala		340	345	350		att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104	Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380	
220																																																																																			
tct gct gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720																																																																																		
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys																																																																																			
225	230	235	240	aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa	768	Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu		245	250	255		act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa	816	Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys		260	265	270		aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga	864	Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly		275	280	285		aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912	Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys		290	295	300		tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960	Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn		305	310	315	320	gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008	Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His		325	330	335		gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056	Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala		340	345	350		att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104	Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380									
235	240																																																																																		
aaa att aca gaa tct aac gca gtt gtt ctg gct gtg aaa gaa att gaa	768																																																																																		
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu																																																																																			
245	250	255		act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa	816	Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys		260	265	270		aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga	864	Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly		275	280	285		aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912	Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys		290	295	300		tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960	Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn		305	310	315	320	gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008	Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His		325	330	335		gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056	Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala		340	345	350		att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104	Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380																	
255																																																																																			
act ttg ctt gca tct ata gat gaa ctt gct act aaa gct att ggt aaa	816																																																																																		
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys																																																																																			
260	265	270		aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga	864	Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly		275	280	285		aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912	Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys		290	295	300		tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960	Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn		305	310	315	320	gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008	Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His		325	330	335		gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056	Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala		340	345	350		att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104	Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380																									
270																																																																																			
aaa ata caa caa aat ggt ggt tta gct gtc gaa gcg ggg cat aat gga	864																																																																																		
Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly																																																																																			
275	280	285		aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912	Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys		290	295	300		tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960	Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn		305	310	315	320	gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008	Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His		325	330	335		gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056	Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala		340	345	350		att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104	Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380																																	
285																																																																																			
aca ttg tta gca ggt gct tat aca ata tca aaa cta ata aca caa aaa	912																																																																																		
Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys																																																																																			
290	295	300		tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960	Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn		305	310	315	320	gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008	Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His		325	330	335		gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056	Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala		340	345	350		att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104	Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380																																									
300																																																																																			
tta gat gga ttg aaa aat tca gaa aaa tta aag gaa aaa att gaa aat	960																																																																																		
Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn																																																																																			
305	310	315	320	gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008	Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His		325	330	335		gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056	Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala		340	345	350		att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104	Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380																																																	
315	320																																																																																		
gct aag aaa tgt tct gaa gat ttt act aaa aaa cta gaa gga gaa cat	1008																																																																																		
Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His																																																																																			
325	330	335		gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056	Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala		340	345	350		att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104	Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380																																																									
335																																																																																			
gcg caa ctt gga att gaa aat gtt act gat gag aat gca aaa aaa gct	1056																																																																																		
Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala																																																																																			
340	345	350		att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104	Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu		355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380																																																																	
350																																																																																			
att tta ata aca gat gca gct aaa gat aag ggc gct gca gag ctt gaa	1104																																																																																		
Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu																																																																																			
355	360	365		aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152	Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met		370	375	380																																																																									
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aag cta ttt aaa gca gta gaa aac ttg gca aaa gca gct aaa gag atg	1152																																																																																		
Lys Leu Phe Lys Ala Val Glu Asn Leu Ala Lys Ala Ala Lys Glu Met																																																																																			
370	375	380																																																																																	
380																																																																																			

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ctt gct aat tca gtt aaa gag ctt ac
 Leu Ala Asn Ser Val Lys Glu Leu
 385 390

1178

<210> 74
 <211> 392
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 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80
 Ala Thr Lys Ala Ile Gly Lys Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160
 Asn Ala Gln Arg Ala Ile Leu Lys Lys His Ala Asn Lys Asp Lys Gly
 165 170 175
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
 180 185 190
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Ile Val His Gly Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn
 210 215 220
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 225 230 235 240
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu
 245 250 255
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
 260 265 270

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Lys Ile Gln Gln Asn Gly Gly Leu Ala Val Glu Ala Gly His Asn Gly
 275 280 285
 Thr Leu Leu Ala Gly Ala Tyr Thr Ile Ser Lys Leu Ile Thr Gln Lys
 290 295 300
 Leu Asp Gly Leu Lys Asn Ser Glu Lys Leu Lys Glu Lys Ile Glu Asn
 305 310 315 320
 Ala Lys Lys Cys Ser Glu Asp Phe Thr Lys Lys Leu Glu Gly Glu His
 325 330 335
 Ala Gln Leu Gly Ile Glu Asn Val Thr Asp Glu Asn Ala Lys Lys Ala
 340 345 350
 Ile Leu Ile Thr Asp Ala Ala Lys Asp Lys Gly Ala Ala Glu Leu Glu
 355 360 365
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<220>
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 1 5 10 15

gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca gga aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30

gat ggg aat gca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca gtt gtt 192
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60

ctg gcc gtg aaa gaa gtt gag acc tta ctt gca tct ata gat gaa ctt 240
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80

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gct acc aaa gct att ggt aaa aaa ata ggc aat aat ggt tta gag gcc	288		
Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala			
85	90	95	
aat cag agt aaa aac aca tca ttg tta tca gga gct tat gca ata tct	336		
Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser			
100	105	110	
gac cta ata gca gaa aaa tta aat gta ttg aaa aat gaa gaa tta aag	384		
Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys			
115	120	125	
gaa aag att gat aca gct aag caa tgt tct aca gaa ttt act aat aaa	432		
Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys			
130	135	140	
cta aaa agt gaa cat gca gtg ctt ggt ctg gac aat ctt act gat gat	480		
Leu Lys Ser Glu His Ala Val Leu Gly Leu Asn Leu Thr Asp Asp			
145	150	155	160
aat gca caa aga gct att tta aaa aaa cat gca aat aaa gat aag ggt	528		
Asn Ala Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys Gly			
165	170	175	
gct gca gaa ctt gaa aag tta ttt aaa gcg gta gaa aac tta tca aaa	576		
Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys			
180	185	190	
gca gct caa gac aca tta aaa aat gct gtt aaa gag ctt aca agt cct	624		
Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro			
195	200	205	
att gtc cat ggt aat aat tca aga aaa gat ggg aat gca tct aca aat	672		
Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn			
210	215	220	
tct gcc gat gag tct gtt aaa ggg cct aat ctt aca gaa ata agt aaa	720		
Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys			
225	230	235	240
aaa att aca gaa tct aac gca gtt gtt ctg gcc gtg aaa gaa gtt gag	768		
Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu			
245	250	255	

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acc tta ctt gca tct ata gat gaa ctt gct acc aaa gct att ggt aag	816		
Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys			
260	265	270	
aaa ata ggc aat aat ggt tta gag gcc aat cag agt aaa aac aca tca	864		
Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser			
275	280	285	
ttg tta tca gga gct tat gca ata tct gac cta ata gca gaa aaa tta	912		
Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu			
290	295	300	
aat gta ttg aaa aat gaa gaa tta aag gaa aag att gat aca gct aag	960		
Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys			
305	310	315	320
caa tgt tct aca gaa ttt act aat aaa cta aaa agt gaa cat gca gtg	1008		
Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val			
325	330	335	
ctt ggt ctg gac aat ctt act gat gat aat gca caa aga gct att tta	1056		
Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu			
340	345	350	
aaa aaa cat gca aat aaa gat aag ggt gct gca gaa ctt gaa aag tta	1104		
Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu			
355	360	365	
ttt aaa gcg gta gaa aac tta tca aaa gca gct caa gac aca tta aaa	1152		
Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys			
370	375	380	
aat gct gtt aaa gag ctt aca agt cc	1178		
Asn Ala Val Lys Glu Leu Thr Ser			
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Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	

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Asp Gly Asn Ala Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala Val Val
 50 55 60
 Leu Ala Val Lys Glu Val Glu Thr Leu Leu Ala Ser Ile Asp Glu Leu
 65 70 75 80

 Ala Thr Lys Ala Ile Gly Lys Ile Gly Asn Asn Gly Leu Glu Ala
 85 90 95
 Asn Gln Ser Lys Asn Thr Ser Leu Leu Ser Gly Ala Tyr Ala Ile Ser
 100 105 110
 Asp Leu Ile Ala Glu Lys Leu Asn Val Leu Lys Asn Glu Glu Leu Lys
 115 120 125
 Glu Lys Ile Asp Thr Ala Lys Gln Cys Ser Thr Glu Phe Thr Asn Lys
 130 135 140
 Leu Lys Ser Glu His Ala Val Leu Gly Leu Asp Asn Leu Thr Asp Asp
 145 150 155 160
 Asn Ala Gln Arg Ala Ile Leu Lys His Ala Asn Lys Asp Lys Gly
 165 170 175
 Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu Asn Leu Ser Lys
 180 185 190
 Ala Ala Gln Asp Thr Leu Lys Asn Ala Val Lys Glu Leu Thr Ser Pro
 195 200 205
 Ile Val His Gly Asn Asn Ser Arg Lys Asp Gly Asn Ala Ser Thr Asn
 210 215 220
 Ser Ala Asp Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys
 225 230 235 240
 Lys Ile Thr Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu
 245 250 255
 Thr Leu Leu Ala Ser Ile Asp Glu Leu Ala Thr Lys Ala Ile Gly Lys
 260 265 270
 Lys Ile Gly Asn Asn Gly Leu Glu Ala Asn Gln Ser Lys Asn Thr Ser
 275 280 285
 Leu Leu Ser Gly Ala Tyr Ala Ile Ser Asp Leu Ile Ala Glu Lys Leu
 290 295 300
 Asn Val Leu Lys Asn Glu Glu Leu Lys Glu Lys Ile Asp Thr Ala Lys
 305 310 315 320
 Gln Cys Ser Thr Glu Phe Thr Asn Lys Leu Lys Ser Glu His Ala Val
 325 330 335
 Leu Gly Leu Asp Asn Leu Thr Asp Asp Asn Ala Gln Arg Ala Ile Leu
 340 345 350
 Lys Lys His Ala Asn Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu
 355 360 365
 Phe Lys Ala Val Glu Asn Leu Ser Lys Ala Ala Gln Asp Thr Leu Lys
 370 375 380
 Asn Ala Val Lys Glu Leu Thr Ser
 385 390

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 530 Virginia Road, P.O. Box 9133
 Concord, Massachusetts 01742-9133

<210> 77

<211> 1230

<212> DNA

<213> ospC Chimera

<220>

<221> CDS

<222> (1)...(1230)

<400> 77

atg	aga	tta	tta	ata	gga	ttt	gct	tta	gcg	tta	gct	tta	ata	gga	tgt	48
Met	Arg	Leu	Leu	Ile	Gly	Phe	Ala	Leu	Ala	Leu	Ala	Leu	Ile	Gly	Cys	
1		5						10					15			

gca	caa	aaa	ggt	gct	gag	tca	att	gga	tcc	tgt	aat	aat	tca	ggg	aaa	96
Ala	Gln	Lys	Gly	Ala	Glu	Ser	Ile	Gly	Ser	Cys	Asn	Asn	Ser	Gly	Lys	
20					25						30					

gat	ggg	aat	aca	tct	gca	aat	tct	gct	gat	gag	tct	gtt	aaa	ggg	cct	144
Asp	Gly	Asn	Thr	Ser	Ala	Asn	Ser	Ala	Asp	Glu	Ser	Val	Lys	Gly	Pro	
35					40				45							

aat	ctt	aca	gaa	ata	agt	aaa	aaa	att	acg	gat	tct	aat	gct	gtt	tta	192
Asn	Leu	Thr	Glu	Ile	Ser	Lys	Lys	Ile	Thr	Asp	Ser	Asn	Ala	Val	Leu	
50					55					60						

ctt	gct	gtg	aaa	gag	gtt	gaa	gct	ttg	ctg	tca	tct	ata	gat	gaa	att	240
Leu	Ala	Val	Lys	Glu	Val	Ala	Leu	Leu	Ser	Ser	Ile	Asp	Glu	Ile		
65				70				75			80					

gct	gct	aaa	gct	att	ggt	aaa	aaa	ata	cac	caa	aat	aat	ggt	ttg	gat	288
Ala	Ala	Lys	Ala	Ile	Gly	Lys	Ile	His	Gln	Asn	Asn	Gly	Leu	Asp		
85					90				95							

acc	gaa	tat	aat	cac	aat	gga	tca	ttg	tta	gct	gca	aat				336
Thr	Glu	Tyr	Asn	His	Asn	Gly	Ser	Leu	Leu	Ala	Gly	Ala	Tyr	Ala	Ile	
100				105						110						

tca	acc	cta	ata	aaa	caa	aaa	tta	gat	gga	ttg	aaa	aat	gaa	gga	tta	384
Ser	Thr	Leu	Ile	Lys	Gln	Lys	Leu	Asp	Gly	Leu	Lys	Asn	Glu	Gly	Leu	
115					120					125						

aag	gaa	aaa	att	gat	gct	aag	aaa	tgt	tct	gaa	aca	ttt	act	aat	432
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat			480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa			528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca			576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc			624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca aaa aaa cct ttc cat ggt aat aat tca			672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser			
210	215	220	
ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa gga cct			720
Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro			
225	230	235	240
aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca ttt tta			768
Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu			
245	250	255	
ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat gaa ctt			816
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu			
260	265	270	
tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta gat aac			864
Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn			
275	280	285	
gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa ata tca			912
Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser			
290	295	300	
aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa tta aag			960
Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys			
305	310	315	320

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aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act act aag	1008		
Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys			
325	330		
335			
cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag gat gat	1056		
Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp			
340	345		
350			
aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac aag ggt	1104		
Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly			
355	360		
365			
gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg tca aaa	1152		
Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys			
370	375		
380			
gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca aat cct	1200		
Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro			
385	390		
395	400		
gtt gtg gca gaa agt cca aaa aaa cct taa	1230		
Val Val Ala Glu Ser Pro Lys Lys Pro *			
405			
<210> 78			
<211> 409			
<212> PRT			
<213> ospC Chimera			
<400> 78			
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile			
65	70	75	80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp			
85	90	95	
Thr Glu Tyr Asn His Asn Gly Ser Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu			
115	120	125	

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Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140

 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Phe His Gly Asn Asn Ser
 210 215 220
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys Gly Pro
 225 230 235 240
 Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe Leu
 245 250 255
 Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Leu
 260 265 270
 Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu Asp Asn
 275 280 285
 Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu Ile Ser
 290 295 300
 Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu Leu Lys
 305 310 315 320
 Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr Thr Lys
 325 330 335
 Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln Asp Asp
 340 345 350
 Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp Lys Gly
 355 360 365
 Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu Ser Lys
 370 375 380
 Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr Asn Pro
 385 390 395 400
 Val Val Ala Glu Ser Pro Lys Lys Pro
 405

<210> 79
 <211> 1209
 <212> DNA
 <213> ospC Chimera

 <220>
 <221> CDS
 <222> (1)...(1209)

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 Concord, Massachusetts 01742-9133

<400> 79

atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt	48
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys	
1 5 10 15	
gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa	96
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys	
20 25 30	
gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct	144
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro	
35 40 45	
aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65 70 75 80	
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp	
85 90 95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100 105 110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115 120 125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aat aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576

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Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc			624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca			672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser			
210	215	220	
ggg aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa			720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys			
225	230	235	240
ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca			768
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala			
245	250	255	
gtt gtt ctc gcc gtg aaa gaa gtt gaa act ttg ctt aca tct ata gat			816
Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp			
260	265	270	
gag ctt gct aaa gct att ggt aaa aaa ata aaa aac gat gtt agt tta			864
Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu			
275	280	285	
gat aat gag gca gat cac aac gga tca tta ata tca gga gca tat tta			912
Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu			
290	295	300	
att tca aac tta ata aca aaa aaa ata agt gca ata aaa gat tca gga			960
Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly			
305	310	315	320
gaa ttg aag gca gaa att gaa aag gct aag aaa tgt tct gaa gaa ttt			1008
Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe			
325	330	335	
act gct aaa tta aaa ggt gaa cac aca gat ctt ggt aaa gaa ggc gtt			1056
Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val			
340	345	350	
act gat gat aat gca aaa aaa gcc att tta aaa aca aat aat gat aaa			1104
Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys			
355	360	365	

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act aag ggc gct gat gaa ctt gaa aag tta ttt gaa tca gta aaa aac	1152		
Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn			
370	375		
385	390		
ttg tca aaa gca gct aaa gag atg ctt act aat tca gtt aaa gag ctt	1200		
Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu			
395	400		
aca agc taa	1209		
Thr Ser *			
<210> 80			
<211> 402			
<212> PRT			
<213> ospC Chimera			
<400> 80			
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ile Gly Cys			
1	5	10	15
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys			
20	25	30	
Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro			
35	40	45	
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu			
50	55	60	
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile			
65	70	75	80
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp			
85	90	95	
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile			
100	105	110	
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu			
115	120	125	
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn			
130	135	140	
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp			
145	150	155	160
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys			
165	170	175	
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser			
180	185	190	
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser			
195	200	205	
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser			
210	215	220	

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Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 225 230 235 240
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala
 245 250 255
 Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu Thr Ser Ile Asp
 260 265 270
 Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Val Ser Leu
 275 280 285
 Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser Gly Ala Tyr Leu
 290 295 300
 Ile Ser Asn Leu Ile Thr Lys Lys Ile Ser Ala Ile Lys Asp Ser Gly
 305 310 315 320
 Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys Ser Glu Glu Phe
 325 330 335
 Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly Lys Glu Gly Val
 340 345 350
 Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr Asn Asn Asp Lys
 355 360 365
 Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu Ser Val Lys Asn
 370 375 380
 Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser Val Lys Glu Leu
 385 390 395 400
 Thr Ser

<210> 81
 <211> 1205
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1205)

<400> 81
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 gca caa aaa ggt gct gag tca att gga tcc tgt aat aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa ggg cct 144
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45

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 530 Virginia Road, P.O. Box 9133
 Concord, Massachusetts 01742-9133

aat ctt aca gaa ata agt aaa aaa att acg gat tct aat gcg gtt tta	192
Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Val Leu	
50 55 60	
ctt gct gtg aaa gag gtt gaa gcg ttg ctg tca tct ata gat gaa att	240
Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp Glu Ile	
65 70 75 80	
gct gct aaa gct att ggt aaa aaa ata cac caa aat aat ggt ttg gat	288
Ala Ala Lys Ala Ile Gly Lys Lys Ile His Gln Asn Asn Gly Leu Asp	
85 90 95	
acc gaa tat aat cac aat gga tca ttg tta gcg gga gct tat gca ata	336
Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile	
100 105 110	
tca acc cta ata aaa caa aaa tta gat gga ttg aaa aat gaa gga tta	384
Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu	
115 120 125	
aag gaa aaa att gat gcg gct aag aaa tgt tct gaa aca ttt act aat	432
Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn	
130 135 140	
aaa tta aaa gaa aaa cac aca gat ctt ggt aaa gaa ggt gtt act gat	480
Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp	
145 150 155 160	
gct gat gca aaa gaa gcc att tta aaa aca aat ggt act aaa act aaa	528
Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys	
165 170 175	
ggt gct gaa gaa ctt gga aaa tta ttt gaa tca gta gag gtc ttg tca	576
Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser	
180 185 190	
aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag ctt aca agc	624
Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser	
195 200 205	
cct gtt gtg gca gaa agt cca aaa aaa cct tcc atg gta aat aat tca	672
Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser	
210 215 220	
gga aaa gat ggg aat aca tct gca aat tct gct gat gag tct gtt aaa	720
Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys	
225 230 235 240	

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ggg cct aat ctt aca gaa ata agt aaa aaa att aca gaa tct aac gca	768		
Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser Asn Ala			
245	250	255	
gtt gtt ctg gct gtg aaa gaa att gaa act ttg ctt gca tct ata gat	816		
Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp			
260	265	270	
gaa ctt gct act aaa gct att ggt aaa aaa ata caa caa aat ggt ggt	864		
Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly			
275	280	285	
tta gct gtc gaa gcg ggg cat aat gga aca ttg tta gca ggt gct tat	912		
Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr			
290	295	300	
aca ata tca aaa cta ata aca caa aaa tta gat gga ttg aaa aat tca	960		
Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser			
305	310	315	320
gaa aaa tta aag gaa aaa att gaa aat gct aag aaa tgt tct gaa gat	1008		
Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp			
325	330	335	
ttt act aaa aaa cta gaa gga gaa cat gcg caa ctt gga att gaa aat	1056		
Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn			
340	345	350	
gtt act gat gag aat gca aaa aaa gct att tta ata aca gat gca gct	1104		
Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala			
355	360	365	
aaa gat aag ggc gct gca gag ctt gaa aag cta ttt aaa gca gta gaa	1152		
Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu			
370	375	380	
aac ttg gca aaa gca gct aaa gag atg ctt gct aat tca gtt aaa gag	1200		
Asn Leu Ala Lys Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu			
385	390	395	400
ctt ac	1205		
Leu			

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 Hamilton, Brook, Smith & Reynolds, P.C.
 530 Virginia Road, P.O. Box 9133
 Concord, Massachusetts 01742-9133

<210> 82

<211> 401

<212> PRT

<213> ospC Chimera

<400> 82

Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Asn Asn Ser Gly Lys
 20 25 30
 Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys Gly Pro
 35 40 45
 Asn Leu Thr Glu Ile Ser Lys Ile Thr Asp Ser Asn Ala Val Leu
 50 55 60
 Leu Ala Val Lys Glu Val Ala Leu Leu Ser Ser Ile Asp Glu Ile
 65 70 75 80
 Ala Ala Lys Ala Ile Gly Lys Ile His Gln Asn Asn Gly Leu Asp
 85 90 95
 Thr Glu Tyr Asn His Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala Ile
 100 105 110
 Ser Thr Leu Ile Lys Gln Lys Leu Asp Gly Leu Lys Asn Glu Gly Leu
 115 120 125
 Lys Glu Lys Ile Asp Ala Ala Lys Lys Cys Ser Glu Thr Phe Thr Asn
 130 135 140
 Lys Leu Lys Glu Lys His Thr Asp Leu Gly Lys Glu Gly Val Thr Asp
 145 150 155 160
 Ala Asp Ala Lys Glu Ala Ile Leu Lys Thr Asn Gly Thr Lys Thr Lys
 165 170 175
 Gly Ala Glu Glu Leu Gly Lys Leu Phe Glu Ser Val Glu Val Leu Ser
 180 185 190
 Lys Ala Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu Leu Thr Ser
 195 200 205
 Pro Val Val Ala Glu Ser Pro Lys Lys Pro Ser Met Val Asn Asn Ser
 210 215 220
 Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser Val Lys
 225 230 235 240
 Gly Pro Asn Leu Thr Glu Ile Ser Lys Ile Thr Glu Ser Asn Ala
 245 250 255
 Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser Ile Asp
 260 265 270
 Glu Leu Ala Thr Lys Ala Ile Gly Lys Lys Ile Gln Gln Asn Gly Gly
 275 280 285
 Leu Ala Val Glu Ala Gly His Asn Gly Thr Leu Leu Ala Gly Ala Tyr
 290 295 300
 Thr Ile Ser Lys Leu Ile Thr Gln Lys Leu Asp Gly Leu Lys Asn Ser
 305 310 315 320

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Glu Lys Leu Lys Glu Lys Ile Glu Asn Ala Lys Lys Cys Ser Glu Asp
 325 330 335
 Phe Thr Lys Lys Leu Glu Gly Glu His Ala Gln Leu Gly Ile Glu Asn
 340 345 350
 Val Thr Asp Glu Asn Ala Lys Lys Ala Ile Leu Ile Thr Asp Ala Ala
 355 360 365
 Lys Asp Lys Gly Ala Ala Glu Leu Glu Lys Leu Phe Lys Ala Val Glu
 370 375 380
 Asn Leu Ala Lys Ala Lys Glu Met Leu Ala Asn Ser Val Lys Glu
 385 390 395 400
 Leu

<210> 83
 <211> 1236
 <212> DNA
 <213> ospC Chimera

<220>
 <221> CDS
 <222> (1)...(1236)

<400> 83
 atg aga tta tta ata gga ttt gct tta gcg tta gct tta ata gga tgt 48
 Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys
 1 5 10 15

 gca caa aaa ggt gct gag tca att gga tcc tgt agt aat tca ggg aaa 96
 Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys
 20 25 30

 ggt ggg gat tct gca tct act aat cct gct gac gag tct gcg aaa ggg 144
 Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly
 35 40 45

 cct aat ctt aca gaa ata agc aaa aaa att aca gat tct aat gca ttt 192
 Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 50 55 60

 gta ctt gct gtt aaa gaa gtt gag act ttg gtt tta tct ata gat gaa 240
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
 65 70 75 80

 ctt gct aag aaa gct att ggt caa aaa ata gac aat aat aat ggt tta 288
 Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
 85 90 95

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gct gct tta aat aat cag aat gga tcg ttg tta gca gga gcc tat gca Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala 100 105 110	336
ata tca acc cta ata aca gaa aaa ttg agt aaa ttg aaa aat tta gaa Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu 115 120 125	384
gaa tta aag aca gaa att gca aag gct aag aaa tgt tcc gaa gaa ttt Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe 130 135 140	432
act aat aaa cta aaa agt ggt cat gca gat ctt ggc aaa cag gat gct Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala 145 150 155 160	480
acc gat gat cat gca aaa gca gct att tta aaa aca cat gca act acc Thr Asp Asp His Ala Lys Ala Ile Leu Lys Thr His Ala Thr Thr 165 170 175	528
gat aaa ggt gct aaa gaa ttt aaa gat tta ttt gaa tca gta gaa ggt Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly 180 185 190	576
ttg tta aaa gca gct caa gta gca cta act aat tca gtt aaa gaa ctt Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu 195 200 205	624
aca agt cct gtt gta gca gaa agt cca aaa aaa cct cat atg gct aat Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn 210 215 220	672
aat tca ggt ggg gat tct gca tct act aat cct gat gag tct gca aaa Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys 225 230 235 240	720
gga cct aat ctt acc gta ata agc aaa aaa att aca gat tct aat gca Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala 245 250 255	768
ttt tta ctg gct gtg aaa gaa gtt gag gct ttg ctt tca tct ata gat Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp 260 265 270	816
gaa ctt tct aaa gct att ggt aaa aaa ata aaa aat gat ggt act tta Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu 275 280 285	864

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gat aac gaa gca aat cga aac gaa tca ttg ata gca gga gct tat gaa	912
Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu	
290 295 300	
ata tca aaa cta ata aca caa aaa tta agt gta ttg aat tca gaa gaa	960
Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu	
305 310 315 320	
tta aag aaa aaa att aaa gag gct aag gat tgt tcc caa aaa ttt act	1008
Leu Lys Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr	
325 330 335	
act aag cta aaa gat agt cat gca gag ctt ggt ata caa agc gtt cag	1056
Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln	
340 345 350	
gat gat aat gca aaa aaa gct att tta aaa aca cat gga act aaa gac	1104
Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp	
355 360 365	
aag ggt gct aaa gaa ctt gaa gag tta ttt aaa tca cta gaa agc ttg	1152
Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu	
370 375 380	
tca aaa gca gcg caa gca gca tta act aat tca gtt aaa gag ctt aca	1200
Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr	
385 390 395 400	
aat cct gtt gtg gca gaa agt cca aaa aaa cct taa	1236
Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro *	
405 410	
<210> 84	
<211> 411	
<212> PRT	
<213> ospC Chimera	
<400> 84	
Met Arg Leu Leu Ile Gly Phe Ala Leu Ala Leu Ala Leu Ile Gly Cys	
1 5 10 15	
Ala Gln Lys Gly Ala Glu Ser Ile Gly Ser Cys Ser Asn Ser Gly Lys	
20 25 30	
Gly Gly Asp Ser Ala Ser Thr Asn Pro Ala Asp Glu Ser Ala Lys Gly	
35 40 45	

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Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala Phe
 50 55 60
 Val Leu Ala Val Lys Glu Val Glu Thr Leu Val Leu Ser Ile Asp Glu
 65 70 75 80
 Leu Ala Lys Lys Ala Ile Gly Gln Lys Ile Asp Asn Asn Asn Gly Leu
 85 90 95
 Ala Ala Leu Asn Asn Gln Asn Gly Ser Leu Leu Ala Gly Ala Tyr Ala
 100 105 110
 Ile Ser Thr Leu Ile Thr Glu Lys Leu Ser Lys Leu Lys Asn Leu Glu
 115 120 125
 Glu Leu Lys Thr Glu Ile Ala Lys Ala Lys Lys Cys Ser Glu Glu Phe
 130 135 140
 Thr Asn Lys Leu Lys Ser Gly His Ala Asp Leu Gly Lys Gln Asp Ala
 145 150 155 160
 Thr Asp Asp His Ala Lys Ala Ala Ile Leu Lys Thr His Ala Thr Thr
 165 170 175
 Asp Lys Gly Ala Lys Glu Phe Lys Asp Leu Phe Glu Ser Val Glu Gly
 180 185 190
 Leu Leu Lys Ala Ala Gln Val Ala Leu Thr Asn Ser Val Lys Glu Leu
 195 200 205
 Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro His Met Ala Asn
 210 215 220
 Asn Ser Gly Gly Asp Ser Ala Ser Thr Asn Pro Asp Glu Ser Ala Lys
 225 230 235 240
 Gly Pro Asn Leu Thr Val Ile Ser Lys Lys Ile Thr Asp Ser Asn Ala
 245 250 255
 Phe Leu Leu Ala Val Lys Glu Val Glu Ala Leu Leu Ser Ser Ile Asp
 260 265 270
 Glu Leu Ser Lys Ala Ile Gly Lys Lys Ile Lys Asn Asp Gly Thr Leu
 275 280 285
 Asp Asn Glu Ala Asn Arg Asn Glu Ser Leu Ile Ala Gly Ala Tyr Glu
 290 295 300
 Ile Ser Lys Leu Ile Thr Gln Lys Leu Ser Val Leu Asn Ser Glu Glu
 305 310 315 320
 Leu Lys Lys Ile Lys Glu Ala Lys Asp Cys Ser Gln Lys Phe Thr
 325 330 335
 Thr Lys Leu Lys Asp Ser His Ala Glu Leu Gly Ile Gln Ser Val Gln
 340 345 350
 Asp Asp Asn Ala Lys Ala Ile Leu Lys Thr His Gly Thr Lys Asp
 355 360 365
 Lys Gly Ala Lys Glu Leu Glu Leu Phe Lys Ser Leu Glu Ser Leu
 370 375 380
 Ser Lys Ala Ala Gln Ala Ala Leu Thr Asn Ser Val Lys Glu Leu Thr
 385 390 395 400

Asn Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 405 410

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<210> 85
 <211> 192
 <212> PRT
 <213> borrelia burgdorferi

<400> 85
 Cys Asn Asn Ser Gly Lys Asp Gly Asn Thr Ser Ala Asn Ser Ala Asp
 1 5 10 15
 Glu Ser Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr
 20 25 30
 Glu Ser Asn Ala Val Val Leu Ala Val Lys Glu Val Glu Thr Leu Leu
 35 40 45
 Thr Ser Ile Asp Glu Leu Ala Lys Ala Ile Gly Lys Lys Ile Lys Asn
 50 55 60
 Asp Val Ser Leu Asp Asn Glu Ala Asp His Asn Gly Ser Leu Ile Ser
 65 70 75 80
 Gly Ala Tyr Leu Ile Ser Thr Leu Ile Thr Lys Lys Ile Ser Ala Ile
 85 90 95
 Lys Asp Ser Gly Glu Leu Lys Ala Glu Ile Glu Lys Ala Lys Lys Cys
 100 105 110
 Ser Glu Glu Phe Thr Ala Lys Leu Lys Gly Glu His Thr Asp Leu Gly
 115 120 125
 Lys Glu Gly Val Thr Asp Asp Asn Ala Lys Lys Ala Ile Leu Lys Thr
 130 135 140
 Asn Asn Asp Lys Thr Lys Gly Ala Asp Glu Leu Glu Lys Leu Phe Glu
 145 150 155 160
 Ser Val Lys Asn Leu Ser Lys Ala Ala Lys Glu Met Leu Thr Asn Ser
 165 170 175
 Val Lys Glu Leu Thr Ser Pro Val Val Ala Glu Ser Pro Lys Lys Pro
 180 185 190

<210> 86
 <211> 191
 <212> PRT
 <213> borrelia burgdorferi

<400> 86
 Asn Ser Gly Lys Gly Gly Asn Thr Ser Ala Asn Ser Ala Asp Glu Ser
 1 5 10 15
 Val Lys Gly Pro Asn Leu Thr Glu Ile Ser Lys Lys Ile Thr Glu Ser
 20 25 30
 Asn Ala Val Val Leu Ala Val Lys Glu Ile Glu Thr Leu Leu Ala Ser
 35 40 45

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Ile	Asp	Glu	Leu	Ala	Thr	Lys	Ala	Ile	Gly	Lys	Ile	Gln	Gln	Asn	
50					55					60					
Gly	Gly	Leu	Ala	Val	Glu	Ala	Gly	His	Asn	Gly	Thr	Leu	Leu	Ala	Gly
65				70				75						80	
Ala	Tyr	Thr	Ile	Ser	Lys	Leu	Ile	Thr	Gln	Lys	Leu	Asp	Gly	Leu	Lys
					85				90				95		
Asn	Ser	Glu	Lys	Leu	Lys	Glu	Lys	Ile	Glu	Asn	Ala	Lys	Lys	Cys	Ser
					100			105				110			
Glu	Asp	Phe	Thr	Lys	Lys	Leu	Glu	Gly	Glu	His	Ala	Gln	Leu	Gly	Ile
					115		120				125				
Glu	Asn	Val	Thr	Asp	Glu	Asn	Ala	Lys	Lys	Ala	Ile	Leu	Ile	Thr	Asp
					130		135				140				
Ala	Ala	Lys	Asp	Lys	Gly	Ala	Ala	Glu	Leu	Glu	Lys	Leu	Phe	Lys	Ala
145					150				155				160		
Val	Glu	Asn	Leu	Ala	Lys	Ala	Ala	Lys	Glu	Met	Leu	Ala	Asn	Ser	Val
					165			170				175			
Lys	Glu	Leu	Thr	Ser	Pro	Ile	Val	Ala	Glu	Ser	Pro	Lys	Lys	Pro	
					180			185				190			

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